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Receipt is hereby acknowledged for the following in the U.S. Patent and Trademark Office:

Applicant(s): Finzel et al.
Serial No.: 09/847,670
Filed: May 2, 2001
Title: HEPATITIS C VIRUS HELICASE CRYSTALS,
CRYSTALLOGRAPHIC STRUCTURE AND METHODS

Enclosed: An Information Disclosure Statement (2 pgs); 1449 forms (5 pgs);
copies of 55 documents cited on the 1449 forms; and transmittal document (in
triplicate).

Mailed: January 11, 2002
Docket: 6263.N (M&R 268.62630101)

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A handwritten mark or signature, appearing to be a stylized 'W' or 'J'.

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EXHIBIT A

**INFORMATION
DISCLOSURE
STATEMENT**

Atty. Docket No.: 6263.N	Serial No.: 09/847,670
Applicant(s): Finzel et al.	Confirmation No.: 4815
Filing Date: May 2, 2001	Group: 1645 / 631

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U.S. PATENT DOCUMENTS						
Examiner Initial	Document Number	Date	Name	Class	Subclass	Filing Date Appropriate
CS	6,093,573	07/25/00	Beamer et al.	436	86	

FOREIGN PATENT DOCUMENTS

Examiner Initial	Document Number	Date	Country	Class	Subclass	Translation	
						Yes	No
CS	WO 93/02209	02/04/93	PCT WIPo				
	WO 97/15588	05/01/97	PCT WIPo				
	WO 99/36422	07/22/99	PCT WIPo				

OTHER DOCUMENTS (Including Authors, Title, Date, Pertinent Papers, etc.)

Examiner Initial	Document Description
CS	Bartlett et al., "CAVEAT: A Program to Facilitate the Structure-derived Design of Biologically Active Molecules," Molecular Recognition: Chemical and Biological Problems, Royal Society of Chemistry, Special Pub. No. 78:182-196 (1989).
	Blundell, T.L. and Johnson, N.L., Protein Crystallography, Academic Press, title page, publication page, and table of contents only (8 pages total) (1976).
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↓	Brünger, "Free R value: a novel statistical quantity for assessing the accuracy of crystal structures," Nature. 1992;355:472-5.

EXAMINER	Date Considered
	7/10/03
*Examiner: Initial if citation considered, whether or not citation is in conformance with MPEP 609; Draw line through citation if not in conformance and not considered. Include copy of this form with next communication to applicant.	

EXHIBIT B

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Atty. Docket No.: 6263.N	Serial No.: 09/847,670
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Filing Date: May 2, 2001	Group: 1645 (63)

Examiner Initial	TRADEMARK OFFICE	Document Description
CS		Brünger, "A system for crystallography and NMR," X-PLOR Manual, Version 3.1, Yale University Press, New Haven, CT (1992) (title page, publication page, and table of contents only (13 pages)).
		Cho et al., "Crystal structure of RNA helicase from genotype 1b hepatitis C virus. A feasible mechanism of unwinding duplex RNA," <i>J. Biol. Chem.</i> 1998; 273(24):15045-52.
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		Collaborative Computational Project, No. 4, "The CCP4 suite: programs for protein crystallography" <i>Acta Cryst.</i> 1994;D50:760-3.
		Eisen et al., "HOOK: a program for finding novel molecular architectures that satisfy the chemical and steric requirements of a macromolecule binding site," <i>Proteins: Structure, Function, and Genetics.</i> 1994;19(3):199-221.
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		Gillet et al., "SPROUT: a program for structure generation," <i>J. Comput. Aided Mol. Des.</i> 1993;7(2):127-53.
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		Gorbalyena et al., "Helicases: amino acid sequence comparisons and structure-function relationships," <i>Current Opin. in Struct. Biol.</i> 1993;3:419-429.
		Grakoui et al., "Characterization of the hepatitis C virus-encoded serine proteinase: determination of proteinase-dependent polyprotein cleavage sites," <i>J. Virol.</i> 1993;67(5):2832-43.
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Carly S.

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Examiner Initials	Document Description
CS MAY 07 2003 PATENT & TRADEMARK OFFICE	Hendrickson et al., "Selenomethionyl proteins produced for analysis by multiwavelength anomalous diffraction (MAD): a vehicle for direct determination of three-dimensional structure," <i>EMBO J.</i> 1990;9(5):1665-72.
IC109 TECH CENTER	Houghton, M., in <i>Fields virology</i> , eds., Fields et al., Raven Press, New York, NY, Third Ed., Vol. 1, pp. 1035-1058 (1996).
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	Lauri et al., "CAVEAT: a program to facilitate the design of organic molecules," <i>J. Comput. Aided Mol. Des.</i> 1994;8(1):51-66.
✓	Martin, "3D database searching in drug design," <i>J. Med. Chem.</i> 1992; 35(12):2145-54. Review.

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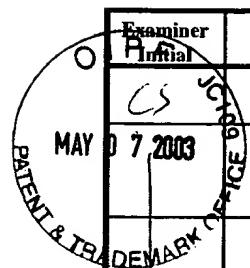
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Examiner Initial	Document Description
CS	Matthews, "Solvent content of protein crystals," <i>J. Mol. Biol.</i> 1968;33(2):491-7.
MAY 07 2003	Meng et al., "Automated Docking with Grid-Based Energy Evaluation," <i>J. Comp. Chem.</i> , 1992;13(4):505-524.
TRADEMARK OFFICE	Miranker et al., "Functionality maps of binding sites: a multiple copy simultaneous search method," <i>Proteins: Structure, Function, and Genetics.</i> 1991;11(1):29-34.
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V	Tong et al., "The locked rotation function," <i>Acta Crystallogr.</i> 1990;A46:783-92.

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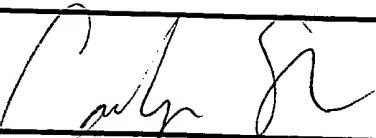
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CS MAY 07 2003 SC109 E.W.	Walker et al., "Distantly related sequences in the alpha- and beta-subunits of ATP synthase, myosin, kinases and other ATP-requiring enzymes and a common nucleotide binding fold," <i>EMBO J.</i> 1982;1(8):945-51.
TD40FMAK/NFME	Wriggers et al., "Protein domain movements: detection of rigid domains and visualization of hinges in comparisons of atomic coordinates," <i>Proteins: Structure, Function, and Genetics.</i> 1997;29(1):1-14.
	Wyckoff et al., eds., <i>Methods in Enzymology, Vol. 114 - Diffraction Methods for Biological Macromolecules</i> , Academic Press, Orlando, FL, title page, publication page, and table of contents only, 5 pages total (1985).
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